

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 19, 2003, 15:28:35 ; Search time 6310 Seconds

(without alignments)
4907.859 Million cell updates/sec

Title: US-09-494-297-2
Perfect score: 3945
Sequence: 1 MKKTRFPNKLNTLQFVLS.....IAGISLGIMGHIRIRKHD 757

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n_model -DEV=xlp
-O=/cgn2_1/USPRO.spool/US09494297/runat_13082003_122946_28092/app_query.fasta_1.903
-DB=GenEmbl -GPM=fastap -SUFFIX=rgc -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=Dlosum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09494297_CGN_1_1_4617_etunal_13082003_122946_28092 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEODDERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl:*
1: gb_da:*
2: gb_htg:*
3: gb_in:*
4: gb_cm:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
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22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*

29: em_vl:*
30: em_htg_hum:*
31: em_htg_in:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3945	100.0	11289	1 AE006482	AE006482 Streptococcus
2	3943	99.9	2400	1 AB083107	AB083107 Streptococcus
3	2058.5	52.2	16207	1 AF447492	AF447492 Streptococcus
4	1965.5	49.8	10826	1 SF043937	SF043937 Streptococcus
5	1862	47.2	52900	1 AE014138	AE014138 Streptococcus
6	1862	47.2	311620	1 AP005141	AP005141 Streptococcus
7	1254.5	31.8	11420	1 AE009963	AE009963 Streptococcus
8	633.5	16.1	2845	1 SRRPRTNE	L10919 Streptococcus
9	611	15.5	2801	1 AF009908	AF009908 Streptococcus
10	603	15.3	2263	1 SPSEFB	X67947 S. pyogenes
11	523	13.3	2066	1 GG031115	U31115 Group G str
12	272.5	6.9	321	1 AF009914	AF009914 Streptococcus
13	262.5	6.7	313	1 AF009913	AF009913 Streptococcus
14	241.5	6.1	326	1 AF009910	AF009910 Streptococcus
15	224.5	5.7	11264	1 AE009964	AE009964 Streptococcus
16	223	5.7	2202	1 AB084272	AB084272 Streptococcus
17	222.5	5.6	348	1 AF009920	AF009920 Streptococcus
18	211.5	5.4	278	1 AF009917	AF009917 Streptococcus
19	211.5	5.4	310	1 AF009911	AF009911 Streptococcus
20	210.5	5.3	309	1 AF009918	AF009918 Streptococcus
21	209.5	5.3	309	1 AF009915	AF009915 Streptococcus
22	207	5.2	301488	1 AE016950	AE016950 Enterococcus
23	205.5	5.2	282	1 AF009912	AF009912 Streptococcus
24	204.5	5.2	308	1 AF009919	AF009919 Streptococcus
25	203.5	5.2	54310	1 AP003515	AP003515 Clostridium
26	202.5	5.1	281	1 AF009909	AF009909 Streptococcus
27	200	5.1	301665	1 AE017009	AE017009 Bacillus
28	185	4.7	255	1 AF009916	AF009916 Streptococcus
29	180	4.6	2127	1 SEFNZEN	X99995 S. equi finz
30	178	4.5	2694	1 AR083961	AR083961 Sequence
31	178	4.5	7650	6 AR083960	AR083960 Sequence
32	178	4.5	8946	1 AF043131	AF043131 Moraxella
33	177	4.5	49617	6 AF067453	AF067453 Sequence
34	176	4.5	2718	1 AF043133	AF043133 Moraxella
35	175.5	4.4	1887	1 AF360373	AF360373 Streptococcus
36	171	4.4	301289	1 AE017000	AE017000 Bacillus
37	170.5	4.3	304708	1 AE017001	AE017001 Bacillus
38	168	4.3	300547	1 AE016954	AE016954 Enterococcus
39	164	4.2	3552	1 SF031980	U31980 Streptococcus
40	162.5	4.1	302470	1 AP000092	AP000092 Thermoplasma
41	162	4.1	5189	1 AY049089	AY049089 Streptococcus
42	161	4.1	4161	6 AX415264	AX415264 Sequence
43	161	4.1	4185	6 AX413693	AX413693 Sequence
44	161	4.1	4249	6 AR228645	AR228645 Sequence
45	161	4.1	4359	6 AR228644	AR228644 Sequence

RESULT 1

ALIGNMENTS

AE006482	11289 bp	DNA	linear	BCF 01-JUN-2001
LOCUS				
DEFINITION	Streptococcus pyogenes M1 GAS strain SF370, section 11 of 167 of the complete genome.			
ACCESSION	AE006482 AE004092			
VERSION	AE006482.1 GI:13621422			
KEYWORDS				
SOURCE	Streptococcus pyogenes M1 GAS			
ORGANISM	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Streptococcus.			
REFERENCE	1 (bases 1 to 11289)			
AUTHORS	Ferritelli, J.J., McShan, W.M., Adjic, D., Savic, D., Savic, G., Lyon, K., Primeaux, C., Sezate, S., Surorov, A.N., Kenton, S., Lai, H., Lin, S., Qian, Y., Jia, H.G., Najjar, F.Z., Ren, Q., Zhu, H., Song, L., White, J., Yuan, X., Clifton, S.W., Roe, B.A. and McLaughlin, R.E.			
TITLE	Complete genome sequence of an M1 strain of Streptococcus pyogenes			
JOURNAL	Proc Natl Acad Sci U S A. 98(48):14658-14663 (2001).			
MEDLINE	21192684			
PUBMED	11296296			
REFERENCE	2 (bases 1 to 11289)			
AUTHORS	Ferritelli, J.J., McShan, W.M., Adjic, D., Savic, D., Savic, G., Lyon, K., Primeaux, C., Sezate, S., Surorov, A.N., Kenton, S., Lai, H., Lin, S., Qian, Y., Jia, H.G., Najjar, F.Z., Ren, Q., Zhu, H., Song, L., White, J., Yuan, X., Clifton, S.W., Roe, B.A. and McLaughlin, R.E.			
TITLE	Direct Submission			
JOURNAL	Submitted (10-APR-2001) Department of Microbiology and Immunology, University of Oklahoma Health Sciences Center, 940 SE Young Blvd, Oklahoma City, OK 73104, USA			
FEATURES	Location/Qualifiers			
source	1. 11289			
gene	/organism="Streptococcus pyogenes M1 GAS"			
CDS	/mol_type="genomic DNA"			
gene	/strain="SF370"			
CDS	/serotype="M1"			
gene	/db_xref="taxon:160490"			
CDS	complement(1496..2137)			
gene	/gene="SpY0121"			
CDS	complement(1496..2137)			
gene	/EC_number="2.7.1.113"			
CDS	/note="Best Blastp hit = dbj BA016044.1 (AB030884)			
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CDS	/transl_table=11			
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gene	/db_xref="GI:13621423"			
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gene	DPKKVAFILQIYFLNRKRSIKRAYOANNIILDFEDELFLIKYKNGNATKELD			
CDS	IYQELLANMIEELGEMPKRPDLITIDVSFDKMERIERGRSFEQVDCNPSELOY			
gene	HOVHGEPWYDEYVSPKMKIDGNSLDFVNPQDILATVLMKIDTKLKEHLHLL"			
CDS	complement(2157..3134)			
gene	/gene="SpY0122"			
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gene	/note="Best Blastp hit = gb AAC97155.1 (U49397) unknown			
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gene	VMEIISKGLVNNKTLHLHLIDENHPMSIQLFGDAGLKRADFIOTNTRKAIIV			
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gene	NALAESAGVSAIAMHGRTEOMYTGCHDETATARYSKATKIPFIGNGNVRSDOAK			
CDS	FMTEELGVAVMTEGRAMNPNVLFITINHFEETGOLPDLPEAKKIDIAKDLKRLIN			
gene	LKGETIAYRFRGLAPHYLRGTGAAKVRGASRAETLAEVEAIFETVR"			
CDS	complement(3121..3993)			
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CDS	complement(3121..3993)			
gene	complement(3121..3993)			
CDS	/note="Best Blastp hit = dbj BA030806.1 (AP001507)			
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CDS	/product="putative heat shock protein HSP33"			
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gene	EVLVGPFGMGHFTVYIDYGTGNPVTSTPLTIGEDGFAYLTSEQTPSPAIAGNV			
CDS	LIDENKRVKAGAFVQVLPAGASEERLARYEKRLQEMPAISHLAKSNVADLLEATY			
gene	GDDPYRLSEEPISFQCDOSRERFEALMTLPKADIQAMIDEDKGAETVQCGCTKYO			
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CDS	YCELNAFPFGSLMTIQKRMISQCFTHPEKREYLVLOKLSANVLDLALFKNGSHS			
gene	RPLDFAHSHELSNSSAYRMREALIPILNRFELKSKNIVGSEYRIKYLIALYSKF			
CDS	GIKIVYDLQODKNTIHSFLSHSTHLSFMSSEFSFDYILALSKRHOSFVTLQ			
gene	TRIFQDLKLFVYDSLSKSHDIITFYCOLNEAGADLYLILYIANNFSASLQMTPE			
CDS	EHIRQYCOLFEENDFRLLNPIITLLPNLKEQKASLYVAMLFESKSPLENOHFTPE			
gene	TNLFVSPPYKGNOKLYTSIKTIYEBEMAKLPCKGRDLNHHKHLFCHYVQSLNIOIP			
CDS	LVYVFAASFTNAHLTDSRPRFSKSIDFSYTYLLQDNVQIIPDLKDLVYTHSOL			
gene	IPFVHHHLTKGIAMVAETISDESLTIOELMYQVEKFOADLTKQLT"			
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CDS	ALPNTDFFKIEPDTTVNEDGKFKGVALLNPMKVTYTNISDGGSNRTKAEFDSSE			
gene	VPEKRGVYVYKYTEKIDKVPGVSYDPTSYQVYVLANNEQOKRVATVYVYKREKS			
CDS	KVPIDKNSLSDSTTLTVKKKVSCTGSDRDKRFRGLTIRAKTSKSEKVMLEKTKG			
gene	GQAPVOTESLIDLYHFTLKDGESIVYMLPGVDVYVEDDKTSKRYTNEVSSQD			
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BASE COUNT      3820 a      1844 c      2243 g      3382 t
ORIGIN
Alignment Scores:
Pred. NO.:      2.84e-243      Length:      11289
Score:      3945.00      Matches:      757
Percent Similarity:      100.00%      Conservative:      0
Best Local Similarity:      100.00%      Mismatches:      0
Query Match:      100.00%      Indels:      0
DB:      1      Gaps:      0
US-09-494-297-2 (1-757) x AE006482 (1-11289)
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Db      5896 ATGAAAAAACAGAGTTCCAAATTAAGCTTAATCTTAATACCAAGGCTATTAAAGT 5955
QY      21 LysAsnSerLysArgPheThrValThrLeuValGlyValPheLeuMetIlePheAlaLeu 40
Db      5956 AAAAAGCTCAAAACGATTACTGTCACCTTAAGTGGAGCTTTTATATGATCTTCGCTTG 6015
QY      41 ValThrSerMetValGlyAlaLysThrValPheGlyLeuValGluSerSerThrProAsn 60
Db      6016 GTAACCTCCAGTGGTGGCTGAAGACGCTTTTGGTTAGTAGAATCCTCGACGCAAC 6075
QY      61 AlaIleAsnProAspSerSerSerGluTrpArgTrpArgLysGlyLysSerThrValArg 80
Db      6076 GCAATAAATCCAGATTCAAGTTCCGAATAACAGATGATGATGAATCTTATGCTAAGA 6135
QY      81 GlyHisProLysThrLysGlnPheArgValAlaHisAspLeuArgValAsnLeuGluLys 100
Db      6136 GGGATCATATTTAAACACTTTAGACTACACACGCTTTAAGGCTTAACCTTAGAAGA 6195
QY      101 SerArgSerThrGlnValThrCysPheAsnLeuLysLysAlaPheProLeuGlySerAsp 120
Db      6196 AGTAGAAGTTATCAAGTTTATGCTTTAATTAAAGAAAGCATTTCCCTCGGATCAGAT 6255
QY      121 SerSerValLysLysTrpTrpLysLysHisAspGlyLysSerThrLysPheGluAspTrp 140
Db      6256 AGTAGTGTAAAGAGGTATTAATAAACATGATGATGATGATGATGATGATGATGATGAT 6315
QY      141 AlaMetSerProArgGlyThrGlyAspGluLeuAsnGlnLysLysLeuArgAlaValMetTrp 160
Db      6316 GCGATGAGCCCTAGAAATTACGCGAGATGAGCTTAATCGAAGCTTAGCGCTTAGTAT 6375
QY      161 AsnGlyHisProGlnAsnAlaAsnGlyLysMetGluLysLeuGluProLeuAsnAlaIle 180

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Db      6376 AATGACATCCACAAATATCCAGATGATATGAGAGCTTGAAACCTTGATGATCTATC 6435
QY      181 ArgValThrGlnGluAlaValTrpTrpTrpSerAspAsnAlaProIleSerAsnProAsp 200
Db      6436 AGAGTTACCAAGAGGCGGATGAGTATCTATGCTATGCTATGCTATGCTATGCTATGCTAT 6495
QY      201 GluSerPheLysArgGluSerGluSerAsnLeuValSerThrSerGlnLeuSerLeuMet 220
Db      6496 GAACTTTTAAAGGAGATCCAGAAAGTAACTTGCTGATCTACTTCCATTTATCTTGTATG 6555
QY      221 ArgGlnAlaLeuLysGlnLeuIleAspProAsnLeuAlaThrLysMetProLysGlnVal 240
Db      6556 GGTCAAGCTTTGAAGCAACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 6615
QY      241 ProAspAspPheGlnLeuSerThrLysLeuSerGluLysAspLysGlyAspLysTrpAsnLys 260
Db      6616 CCGATGATTTTTCACCTAAGTATTTTATGCTGAGGACAAAGGAGATTAATATATATAA 6675
QY      261 GlyTrpGlnAsnLeuLeuSerGlyGlyLeuValProThrLysProProThrProGlyLysP 280
Db      6676 GGATACCAAAATCTTTTATGATGCTGCTTACTTCTTAAACCAACCACTCCAGAGAC 6735
QY      281 ProProMetProProAsnGlnProGlnThrThrSerValLeuIleArgLysThrAlaIle 300
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QY      341 GlyThrTrpThrLeuThrGluLeuAsnSerProAlaGlyTrpSerIleAlaGluProIle 360
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QY      361 ThrPheLysValGluAlaGlyLysValThrThrIleIleAspGlyLysGlnIleGluAsn 380
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QY      401 SerValLeuThrThrGlnAsnThrAlaLysPheTrpTrpAlaLysAsnLysAsnGlySer 420
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QY      421 SerGlnValValThrCysPheAsnAlaAspLeuLysSerProProAspSerGluAspGly 440
Db      7156 TCACAGGTGTCTATGCTTAAATGACAGATCTAAATCTCCACGACTCTGAAATGATGT 7215
QY      441 GlyLysThrMetThrProAspPheThrThrGlyGluValLysTrpThrHisIleAlaGly 460
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QY      461 ArgAspLeuPheLysTrpThrValLysProArgAspThrAspProAspThrPheLeuLys 480
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QY      481 HisIleLysLysValIleGluLysGlyTrpArgGlyLysGlyGlnAlaIleGluTrpSer 500
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QY      501 GlyLeuThrGluThrGlnLeuArgAlaAlaThrGlnLeuAlaIleTrpTrpPheThrAsp 520
Db      7396 GGTCAACTGAGACAACTTCGCTGCGGCTACTGATGATGACAAATATATATTATTCAGTAT 7455
QY      521 SerAlaGluLeuAspLysAspLysLysLysAspTrpHisGlyPheGlyAspMetAsnAsp 540
Db      7456 AGTGCTGAATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGAT 7515

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QY	541	SerThrLeuAlaValAlaLysIleLeuValGluTrpAlaGlnAspSerAspProGln	560
Db	7516	AGTACTTACGAGTGGCTAAATCTCTGTACAAACGCTCAGATAGTAATCTCCACAG	7575
QY	561	LeuThrAspLeuAspPhePheIleProAsnAsnAsnLysTrpGlnSerLeuIleGlyThr	580
Db	7576	CTAAGTACCTTGATTCCTTATATCCGAATACAAATTAATCAATCTCTATTTGGAAT	7635
QY	581	GlnTrpHisProGluAspLeuValAspIleLeuArgMetGluAspLysGluValIle	600
Db	7636	CAGGCGATCCAGAGATTAAGTTGATTAATTTGTAATGAGATTAAGAAAGAAATATA	7695
QY	601	ProValThrHisAsnLeuThrLeuArgLysThrValThrGlyLeuAlaGlyAspArgThr	620
Db	7696	CCCTAAGTCACTAATTTTAACCTTACAGAAAACGGTGCAGCTTACCTGGGACAGAACT	7755
QY	621	LysAspPheHisPheGluIleGluLeuLysAsnAsnLysGlnLysLeuLeuSerGlnThr	640
Db	7756	AAAGATTTCATTTTGAATTTGAATTAAGAAATTAAGCAAGAAATTCCTTCCAAACT	7815
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VERSION			
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REFERENCE	1 Miyoshi-Akiyama, T., Wakisaka, N., Zhao, J. and Uchiyama, T.		
AUTHORS	Characterization of collagen binding protein (cpa) of M1-type group A streptococcus		
TITLE	Unpublished		
JOURNAL	2 (bases 1 to 2400)		
REFERENCE	Miyoshi-Akiyama, T., Wakisaka, N., Zhao, J. and Uchiyama, T.		
AUTHORS	Submitted (03-APR-2002) Tohru Miyoshi-Akiyama, Tokyo Women's		
TITLE	Medical University, Department of Microbiology and Immunology; 8-1,		
JOURNAL	Kawada-cho, Shinjuku-ku, Tokyo 162-8666, Japan		
	(E-mail: kfo01112@nifty.ne.jp; Tel: 81-3-3353-8111 (ex. 22713),		
	Fax: 81-3-5269-7411)		
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 1 (bases 1 to 16207)
 Bessen, D. E. and Kalla, A.
 Genomic localization of a T serotype locus to a recombinatorial zone encoding extracellular matrix-binding proteins in Streptococcus pyogenes
 Infect. Immun. 70 (3), 1159-1167 (2002)
 JOURNAL
 MEDLINE
 21843101
 PUBMED
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 2 (bases 1 to 16207)
 Bessen, D. E. and Kalla, A.
 REFERENCES
 AUTHORS
 TITLE
 Direct Submission
 JOURNAL
 Submitted (12-NOV-2001) Epidemiology & Public Health, Yale

FEATURES University, 60 College Street, New Haven, CT 06520, USA
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Percent Similarity: 71.24% Conservative: 126
Best Local Similarity: 54.30% Mismatches: 189
Query Match: 52.18% Indels: 25
DB: 1 Gaps: 10

US-09-494-297-2 (1-757) x AF447492 (1-16207)

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TITLE
JOURNAL

Direct Submission
Submitted (14-JUN-2002) Laboratory of Human-Bacterial Pathogenesis,
Rocky Mountain Laboratories, NIAID, NIH, 903 South Fourth St.,
Hamilton, MT 59840, USA

FEATURES
source

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951. 1985

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951. 1985

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1987. 2313

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1987. 2313

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2273. 2716

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2273. 2716

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2673. 2957

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2673. 2957

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2950. 3384

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2950. 3384

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3368. 3694

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3368. 3694

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3792. 4745

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4804. 6000

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from Bacillus subtilis [lactococcus lactis subsp.

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VERSION	AP005141.1	GI:28810157	
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SOURCE			
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	Streptococcus pyogenes SSI-1		
	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;		
	Streptococcus.		
REFERENCE	1		
AUTHORS	Nakagawa, I., Kurokawa, K., Yamashita, A., Nakata, M., Tomiyasu, Y.,		
	Okahashi, N., Kawabata, S., Yamazaki, K., Shiba, T., Yasunaga, T.,		
	Hayashi, H., Hattori, M. and Hamada, S.		
TITLE	Genome Sequence of an M3 Strain of Streptococcus pyogenes Reveals a		
	Large-Scale Genomic Rearrangement in Invasive Strains and New		
	Insights into Phage Evolution		
JOURNAL	Genome Res. 13 (6), 1042-1055 (2003)		
MEDLINE	22683278		
REFERENCE	2 (bases 1 to 311600)		
AUTHORS	Yamazaki, A., Nakagawa, I., Kurokawa, K., Nakata, M., Tomiyasu, Y.,		
	Yamazaki, K., Okahashi, N., Kawabata, S., Yasunaga, T., Hattori, M.,		
	Hayashi, H. and Hamada, S.		
TITLE	Direct Submission		
JOURNAL	Submitted (01-MAY-2002) Ken Kurokawa, Osaka University, Genome		

Information: Research Center; 3-1, Yamadaoka, Suita, Osaka 565-0871
Japan (E-mail: kengen-info.osaka-u.ac.jp,
URL: <http://www.gen-info.osaka-u.ac.jp/>, Tel: 81-6-6879-8365,
Fax: 81-6-6879-2047)
Genome Project
This clone was isolated from a patient presenting with toxic shock
like syndrome.

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Db	112429	AATCGATGTCCCGCAAAATTATCAGTTAGTATTTTTCATCTTCATGAT	112476
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D		113293	AACAAAGGGATTATCATGTTTGTGATAAACCAGTAGAACCACTTAAGTCATGAG	113352
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D		113353	TTGATCACCATTACTGCTAGGATGTCACCTTACCCATAGACTCAAAATAGATTCTTTGTT	113412
OY		569	ProAsnAsnAsnLysTyrcInserLeuIleGlyThrGlnTrpHisProGluAspLeuVal	588
D		113413	CCTAATTAGCAGATAGATAGATACAGGCACCTTATTGGAAACGATATCATCAATGAATTGATT	113472
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D		113473	GATGTTATTCTATGAGAAATAAACAGCGCTCCATTATTCCTTTACTCAAGAATTAACT	113523
OY		608	LeuArgLysThrValThrGlyLeuAlaGlyAspArgThrLysAspPheHisPheGluIle	627
D		113533	ATTTCCTAAACGTGTTACTGGAACTATTGCAGATAAAGAAAAAATTAATCTTGGAAATA	113592
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D		113593	CATTTAATAATCTTCTGATGGACAAGCTATTAAGTGAACATATCCGACAACTCTGGAGAA	113655
OY		648	IeuGluPheLysAspGlyLysAlaThrIleAsnLeuLysHisGlyClnSerLeuThrLeu	667
D		113653	CTCACAGTTACAGATGCAAAACCTACTTCCATTAAGAGATGAGAAATCATGATTGTT	113712
OY		668	GlnGlyLeuProGlnLysSerTyrrLeuValLysGluThrAspSerGlnGlyTyrrLys	687
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D		113833	GATGAGACTGAGCTTTGAAAAACCGAAAAAGATCTTGCCACCACTGCTTT-GACAAAC	113891
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ACCESSION		AE009963	AE009949	
VERSION		AE009963.1	GI:19747394	
SOURCE				
ORGANISM			Streptococcus pyogenes MGAS232 Streptococcus pyogenes MGAS232 Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Streptococcus.	
REFERENCE			1 (bases 1 to 11420)	
AUTHORS			Smoot,J.C., Barblian,K.D., Van Gompel,J.J., Smoot,L.M., Chaussee,M.S., Sylva,G.L., Studevant,D.E., Ricklefs,S.M., Porella,S.F., Parkins,L.D., Beres,S.B., Campbell,D.S., Smith,T.M., Zhang,Q., Kapur,V., Daly,J.A., Veasey,L.G. and Musser,T.M.	
TITLE			Genome sequence and comparative microarray analysis of serotype M18 group A Streptococcus strains associated with acute rheumatic fever outbreaks	
JOURNAL			Proc. Natl. Acad. Sci. U.S.A. 99 (7), 4668-4673 (2002)	
MEDLINE			21972593	
PUBMED			11917108	
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AUTHORS			Smoot,J.C., Barblian,K.D., Van Gompel,J.J., Smoot,L.M., Chaussee,M.S., Sylva,G.L., Studevant,D.E., Ricklefs,S.M.,	

Porcella, S.F., Parkins, L.D., Beres, S.B., Campbell, D.S., Smith, T.M., Zhang, Q., Kapur, V., Daly, J.A., Yeasty, L., George, and Musser, J.M.
 Submitted (31-JAN-2002) Laboratory of Human Bacterial Pathogenesis/Rocky Mountain Laboratories/NIH/NIH, 903 S. 4th St., Hamilton, MT 59840, USA
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Length:	.
Matches:	254
Conservative:	69
Mismatches:	129
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US-09-494-297-2 (1-757) x AE009963 (1-11420)

[illegible]

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LOCUS	streptococcus pyogenes		
DEFINITION	complete cds.		
ACCESSION	L10919.1	GI:425479	
VERSION	L10919.1		
KEYWORDS	adenosin; fibronectin-binding protein; protein F; prfF gene.		
SOURCE	Streptococcus pyogenes		


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DB      789  GAAAGTAGAGCTCTATGTTATGTAATAAATTAGATGAGAGTACAGAAACTTTAAATA 848
QY      140  TYRALMETSERPROARGILETHRGYASPGULMEASNGLINLSLEUARGALVALMET
DB      849  TAGCGTGAAGAACCTGAGTTTACTGAGAGGAAATTAAGACGACATATATGAAAGCTTCTC 908
QY      160  TYRASNGLYHISPROGLINASNALASNGLYLLEMETGLUGLYLEUGLUPROLEUASNALA
DB      909  TACAAATGATATCTCT--AATAGTAAATGAATATAGAGGGATAGACCTCTCAACGCT 965
QY      180  ILEARGVALTHRGINGLUALAVALTRPYRTRYRSEASPSANLAPROILESERANPRO
DB      966  ATCTTGATACAGAAATGCGCATATGCTATTACTCGGATRGTCCAGCATTAATGATATT 1025
QY      200  ASPGLUSERPHELYSARGLUSERGLUSERASNLEUVALSERTHYRSEGLINLEUSERLEU
DB      1026  AATAACTCTCTTACTGATGAGCCATGATCTTAATATACCCAGCTCAGCATACGTTA 1085
QY      220  METARGGLINALEULYSGLINLEULE-----ASPPROASNLEUALATHIRYSMETPRO
DB      1086  ATGCGTGAAGCTGTGGAAGAACTAATTTCTCTGAGAAATTTGGTT----- 1133
QY      238  LYSGLINVALPROASPSAPHEGLINLEUSERLIEPHEGLUSERGLUSPLYSGLYASPLYS
DB      1134  AAACAGTTCACAGCACTTAATTAAGTATTTTGAAGTCTCTGAT----- 1181
QY      258  TYRASNLYSGLYTRYGINASNLEULENLEUSERGLYLEUVALPROTHIRYSPROPROTH
DB      1182  ----AGCTCCACCAAAATCTTTAAGTGTGATATGATGATGATGATGATGATGATGAT 1235
QY      278  PROGLYASP----- 280
DB      1236  CCTGGATGATACGTGAGACATATACTCTAAACTCCGAGTGGATGAGCCATTCCTCC 1295
QY      281  -----ProPROMETPROPROASNGINPROGLIN 289
DB      1296  GAGGACCCAAACGTCACAGATGAGCTTCAGGACCTCGCTCCCATTTGATGCCAGAG 1355
QY      290  THIRTHSERVALLEULEARGLYSTRALALEGLYASPTYRSEIRYSEIRYSEULEUGLUGLY
DB      1356  CTAGATGTGAGAGAGTCCAGAAAGTTCACAGCGAGCTTAGAACCTGCGCTTCCCA 1415
QY      310  ALATHLEUGLINLEUHRGLYASPAANVALASERPHLEGINALARGVALPHESESER
DB      1416  TTGGTCCAGAGCTGATGAGTGAAGAGTCCAGAAAGTCCAGC----- 1460
QY      330  ASNAPDILEGLYGLUARGYLEGLULEUSER-----ASPLY 341
DB      1461  -----GAGAGCTTAGAAGCTCGCTTCCCATTTAATGCCAGAGCTAGATGGC 1508
QY      342  THIRYRTHLEUHRGLULEUASNSEPROALAGLYTYRSEIRLEALAGLUPROILETHR
DB      1509  ---CAAGAGTCCCAAGAGTCCAGAGCTGAGAGCTTAGAACCTCGCTTCCATTAAG 1565
QY      362  PHELYSVALGLUALAGLYSVALTYRTHIRLE----- 372
DB      1566  CCAGAGCTAGAGCGTGAAGAAATCCAGAGAGTTCACAGCGAGAGCTTAGAACCTCGCCTT 1625
QY      373  -----ILEASPLYLSGLINLE-----GLUASNPROASNLYSGLULE 385
DB      1626  CCTCCATTATGCCAGAGTTAGATGCTCAAGAGAGTCCGTGAAGAAACCTAGATTATGACTTA 1685

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QY      386  VALGLUPROTYRSEYERVALGLUALATYRASNASPHEGLUGLUPHESEVALLEUTHRTH
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DB      1709  ----- 1709
QY      426  CYSYPHEASNALASPLEULYSSETPROASPSERGLUASPOLYGLYSTRYTHMETTHR
DB      1710  ----TTTAACATATAACCAATACCTCTAGCGGGTAG----- 1745
QY      446  PROASPSERHETHRGYGLUVALLYSTRY--THIRHISILEALAGLYARG----- 461
DB      1746  -----TCTGCTGAGAGCGATTTATATATGCAAGTATATGCAATCAACAGAAC 1793
QY      462  ----ASPLEUPHELYSTRYTHIRVALLYSPROARGASPTTHASPROKSPHTRPHELEU
DB      1794  CCGTGTGATATGATATAAAGCTT-----CCGAATGAAGACGTTTTCAGGAATATAG 1847
QY      480  LYSHISILEULYSVALILEGLULYSGLYTRYARGLULYSGLYGIN-----ALALILE 497
DB      1848  GTTGACACAGAAAGACGAAAGAGCCAGAGCTTGATGCGAGCCCAAGTAGAGTCTGTT 1907
QY      498  GLUTYRSEGLYLEUHRGLUTHRGINLEUARGALALATHRGINLEUALALETYRTRY
DB      1908  GAATTTACGAAGAACCTCAACGAGCAGCAGCGGCTCAACA----- 1949
QY      518  PHEHTRASPSEIRLACILEUASPLYASAPLYSLEULYASAPRYHISGLYPHEGLYASP
DB      1950  --ACTTCAGGTTAGACAGAGAGAGAGAGAAAGACCCAGAGAGTGTG--ATGGAGGCT 2003
QY      538  METASNAPSEIRTHIRLEUALAVALALALYSLILEUVALGLUTYRGLINASPSERASN
DB      2004  CAAGAGAGAGCT-----GTGAATTTACGAAGAGAGCT----- 2036
QY      558  PROPROGLINLEUTHRASPLEUASPPHEPHEILEPROASNASNLYSTRYGLINSEIRLEU
DB      2037  -----CAACAGAGCC 2045
QY      578  ILEGLYTHRGINTRPHISPROGLINASPLEUVALASPLILEARGMETGLUASPLYS
DB      2046  ATGAGTGTCAACACAGCTCCTCAG-----GTTGAGACAGAGACAGAGAA 2090
QY      598  GLUVALILEPROVALTHIRHISASNLEUTHIRLEUARGLYSTRYVALTHRGYLEUALAGLY
DB      2091  GAG-----CCANAAGT-----TTGATGGGA 2111
QY      618  ASPARGTHIRLYSAPSPHEHISPHLEGLULILEGLULEULYSASNANLYSGINLEULEU
DB      2112  GGCCAAGAGTACGTCTGTGAATTAG-----AAAGACACTCAACGAGGATGAGC 2162
QY      638  SERGLINTHRVALLYSTRHIRASPLYSRTHIRASNLEUGLUPHELYASPOLYLYSALATHIRLE
DB      2163  GGTCAACAGAGCT-----CCTCAGGTTGAACAGAGACGAGAAAGCCAGAA 2210
QY      658  ASNLEULYHISGLYGLUSERLEUTHIRLEUGLINGLYLEUPROGLINLYTYRSEIRTYRLEU
DB      2211  GTCTTGATGAGAGCTCAAGTAGCTGTGTAATTACAAAGAT----- 2255
QY      678  VALLYSGLUTHRASPSERGLUGLYTRYRLYSVALLYSVALASNSERGLINGLUALAASN
DB      2256  ---ACTCAAGAGGCTCGAGCGGTTTCAGTGAAGACGTGAGCATTTGTAATAGCGCT 2312
QY      698  ALATHIRVALSERLYSTRHGLYTHIRSERASPSGLUTHIRLEUALAHEGLUASNANLYS
DB      2313  CCGAGAGTTA-----GTCTCCATTTTACACATAATGAG 2345
QY      718  -----GLUPROVALVALPRO----- 722
DB      2346  CCCAAGTGGAGAGAGATGGGAAAGCCTACAAAATAATACACTTATCTCTCTGCA 2405
QY      723  THIRGLYVALASPOLINLYSILEASNGLYTRYLEUALALEUALILEVALILEALAGLYLESER
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[illegible]

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QY	40 LeuValThrSerMetValGlyAlaLysThrValPheGlyLeuValGlySerSerThrPro	59					
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QY	60 AsnAlaIleAsnProAspSerSerSerGluTyrThrGlyPyrGlyTyrGlySerTyrVal	79					
DB	292 CATGAGATTGATGCT-----CAAAATCCTGAGTTTCCCTGGTATGCTTATGATTTCTAC--	342					
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QY	140 TyrIleAsnSerPro-----ArgIleThrGlyAspGluLeuAsn	155					
DB	508 TATGCTGATATACCCCGAAGAAAGATTAATGAAGTCCAGAGTATATGATGTAAATTTGAA	567					
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DB	568 AAAATATATTAAGAGTGCATATATATGATATCCGATTAACGGTAATGGAATCATGAG	627					
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DB	628 GGTATTAACCATTAATATGCTATCTTAAGTAACTCAAAATGCGTTTGGTACTATTCGAT	687					
QY	193 AsnAlaProIleSerAsnProAspGluSerPheLysArgGlyGluSerGluSerAsnLeuVal	212					
DB	688 AATTCAGCTATTTTATATCTGATTAATCTTTTACGACGAGCAAGCAAGATCTTAATATA	747					
QY	213 SerThrSerGlnLeuSerLeuMetArgGlnAlaLeuLysGlnLeuIleAspProAsnLeu	232					
DB	748 AAACCTGACGAATTAATCATTAATATGCTGTGATTAAGAAATATGATATCATCAAGTA	807					
QY	233 AlaThrLysMetProLysGlnValProAspAspPheGlnLeuSerIlePheGluSerGlu	255					
DB	808 TCTGAAGAAATCATTTGAACCTGTCATCTACTTATTAAGCATGAATATTTTGCATTCAC	867					
QY	253 AspLysGlyAspLysTyrLysGlyTyrGlnAsnLeuLeuSerGlyGlyLeuValPro	272					
DB	868 GAT-----AAGCTATATCAAAATCTTAAAGCTGAGTGTGTACCA	909					
QY	273 ThrLysProThrProGlyAspProPheMetProProAsnGlnProGlnIleThrSer	292					
DB	910 GAAATATCCCTTAACCTGCTGAA-----ACCCCTGAACATGAGACCAAAATCTCCGAG	966					
QY	293 ValLeuIleArgLysTyrAlaIleGlyAspTyrSerLysLeuGlnGluGlyAlaThrLeu	312					

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Db      964 TTG-----GATGGCCTCCTCAATTCGCCGAAGCCCA-----993
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Db      994 CAACGTCGAACATGTTTGAACCTACGCTCCACCACTG-----1035
QY      333 GlyIuArgIleGluLeuSerAspGlyThrTyThrLeuThrGluLeuAsnSerProAla 352
Db      1036 -----ATGCTAGACGGA---CAAGAGTCCCGCAGATGCCAAGTGAAGC 1077
QY      353 GlyTyrSerIleAlaGluProIleThrPheIysValGluAlaGlyValTyThrIle 372
Db      1078 TTGAACCTGCGCTCCCTCCATGTATGCCAGAGCTAGATGCCAAGAGTCCCAAGATT 1137
QY      373 -----1LeaspGlyLysGln 377
Db      1138 CCAGGAGAGCTTAGAACCTGCGCTCCCATTTGATGCCAGATGATGATGTCAGAA 1197
QY      378 Ile---GluasnProAsnLysGluIle---ValGluProTyrSerValGluAlaTyAsr 395
Db      1198 GTCCCGAAACAACTGATGTTGACTTACCTATGGAAGATCCTGTTATGAGTTTAAAT 1257
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Db      1258 -----AAAGACCAATCACCTCTAGCGGCTGAGTGTGAGAGAGATATTATTCGAA 1311
QY      416 -----AsnLysAsnGly 419
Db      1312 GTTTATGGAATCAACAGAACCTGTTGATATTGATAAAACCTCCGAAATGGAACAGT 1371
QY      420 SerSerGlnValTyThrCysPheAsnAlaAspLeuLysSerProProAspSerGluAsp 439
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QY      440 -----GlyGlyLysThrMetThrProAspPheThr-----Thr 450
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QY      451 Gly-----GluValLysTyThrHisIleAlaGly---460
Db      1471 GGCATGATGTCGTCAAACAACTCCTCAGGTTGAGACAGAACACAGAAAGCCAGAGGTG 1530
QY      461 -----ArgAspLeuPheLysTyThrValLysProArgAspThrAspPro 475
Db      1531 CTGATGGAGGTCGAAGTGAAGTCTGTTGAATTAC-----AAAGTACTCAACA 1581
QY      476 AspThrPheLeuLysHisIleLysValIleGluLysGlyTyTyTyArgGluLysGly---494
Db      1582 GGCATGATGTCGTCAAACAGCTTCTCAGGTTGAGACAGAACATCGAAAGAGCCAGAGGTG 1641
QY      495 -----GlnAlaIleGluTySerGlyLeuThrGluThrGlnLeuArg 508
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QY      509 AlaAlaThrGln-----LeuAlaIleTyr 516
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QY      517 TyrPheThrAspSerAlaGluLeuAspLysAspLysLeuLysAspTyHisGlyPheGly 536
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QY      537 AspMetAsnAspSerThrLeuAlaValAla-----LysIleLeuValGlu 551
Db      1822 GAA-----ACAGTGACCAATGTTGAAGATACCCGTCGGAAGTTAGTTCCAT 1869
QY      552 TyralGluAspSerAsnProGlnLeuThrAsp-----563
Db      1870 TTT-----GACATATATGAGCCCAAGTGAAGAGATATCGGAAAAAGCTTACAAAAAT 1923
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Db      1983 CCT-----TATTTTGTCACTACTTCC 2003
QY      604 HisAsnLeuThrLeuArgLysThrValThrGlyLeuAlaGlyAspArgThrLysAspPhe 623
Db      2004 TATTTTACCTTTTAAACAAACAAACAAATTAAGTCGATGCT---AAAAGTGT 2060
QY      624 HisPheGluIleGluLeuLysAsnAsnLysGlnGluLeuLeuSerGlnThrValLysThr 643
Db      2061 CCATAGAAATA---ATGCCCAATATGCGAATAGTATGATCTGCTACAGTCAAGACA 2117
QY      644 AspLysThrAsnLeuGluPheLysAspGlyLysAlaThrIleAsnLeuLysHisGlyGlu 663
Db      2118 -----AGTTTATTCANAA-----2132
QY      664 SerLeuThrLeuGlnGlyLeuProGluGlyTyrSerTyThrLeuValLysGluThrAspSer 683
Db      2133 -----GGTACTACTTAT-----ACATCT 2150
QY      684 GluGlyTyTyLysValLysValAsnSerGlnVal 695
Db      2151 GATAATAATTAAGCTGACAGATTAATTCAGACCAAGTA 2186

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RESULT 11
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DEFINITION
ACCESSION
VERSION
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AUTHORS
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JOURNAL
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[illegible]

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VERSION	AF009913.1	GI:2267179			
KEYWORDS					
SOURCE	Streptococcus pyogenes Streptococcus pyogenes Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Streptococcus.				
REFERENCE	1. (bases 1 to 313) Katerov,V., Andreev,A., Schalen,C. and Totolian,A.A. Protein F, a fibronectin-binding protein of Streptococcus pyogenes, also binds human fibrinogen: Isolation of the protein and mapping of the binding region Microbiology 144 (Pt 1), 119-126 (1998)				
JOURNAL	9467904				
MEDLINE	2 (bases 1 to 313) Katerov,V.E., Andreev,A.S., Schalen,C. and Totolian,A.A. Submitted (23-JUN-1997) Medical Microbiology, Lund University, Solvegatan 23, Lund 22362, Sweden				
REFERENCE	Location/Qualifiers				
AUTHORS	1. 313				
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US-09-494-297-2 (1-757) x AF009913 (1-313)					
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 SOURCE Streptococcus pyogenes
 ORGANISM Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 Streptococcus.

REFERENCE
 AUTHORS 1 (bases 1 to 326)
 TITLE Katerov,V., Andreev,A., Schalen,C. and Totolian,A.A.
 JOURNAL Protein F, a fibronectin-binding protein of Streptococcus pyogenes,
 MEDLINE also binds human fibrinogen: Isolation of the protein and mapping
 PUBMED of the binding region
 98129085 Microbiology 144 (Pt 1), 119-126 (1998)
 9467904

REFERENCE
 AUTHORS 2 (bases 1 to 326)
 TITLE Katerov,V.E., Andreev,A.S., Schalen,C. and Totolian,A.A.
 JOURNAL Direct Submission
 Submitted (23-JUN-1997) Medical Microbiology, Lund University,
 Solvegatan 23, Lund 22362, Sweden
 Location/Qualifiers

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US-09-494-297-2 (1-757) x AF009910 (1-326)

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 Streptococcus.

REFERENCE
 AUTHORS 1 (bases 1 to 11264)
 TITLE Smoot,J.C., Barbican,K.D., Van Gompel,J.J., Smoot,L.M.,
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 21927593 Zhang,Q., Kapur,V., Daly,J.A., Veasy,L.G. and Musser,J.M.
 11917108 Genome sequence and comparative microarray analysis of serotype M18
 group A Streptococcus strains associated with acute rheumatic fever
 outbreaks
 Proc. Natl. Acad. Sci. U.S.A. 99 (7), 4668-4673 (2002)

REFERENCE
 AUTHORS 2 (bases 1 to 11264)
 TITLE Smoot,J.C., Barbican,K.D., Van Gompel,J.J., Smoot,L.M.,
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 21927593 Zhang,Q., Kapur,V., Daly,J.A., Veasy,L.G. and Musser,J.M.
 11917108 Genome sequence and comparative microarray analysis of serotype M18
 group A Streptococcus strains associated with acute rheumatic fever
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gene

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